Mycobacterium tuberculosis Beijing Genotype, Thailand—Reply to Dr. Prodinger

To the Editor: We read with interest the report on the occurrence of *Mycobacterium tuberculosis* strains of the Beijing genotype in Thailand (1). In contrast to our findings in Vietnam (2), Prodinger et al. found no significant association between the Beijing genotype and either young age or drug resistance (1). However, we have some caveats regarding the comparison of these two studies. First, we restricted our analysis to newly diagnosed patients to avoid confounding by possible differences in relapse rates between

M. tuberculosis genotypes. Second, we excluded confounding by geographic collection site. Although this was not a problem in our study (with 58% of isolates in Hanoi and 53% in Ho Chi Minh City representing the Beijing genotype), it might be in Thailand in view of the reported difference between Thailand and Malaysia. Third, the statistical power of the study in Thailand was limited: a difference of 56% in the group <25 years versus 43% in the category >25 years is potentially important, even if not statistically significant with the given sample size. The power of the Thailand study to demonstrate an association with drug resistance is similarly limited.

Despite these caveats, we agree with Prodinger et al. that the epidemiology of the Beijing genotype strains may vary among Southeast Asian countries. For instance, in Hong Kong we found no association between the Beijing genotype and younger age and a weak association with isoniazid (INH) resistance (3).

Various explanations may account for these differences. For instance, if our hypothesis that the selective advantage of the Beijing genotype in Vietnam is due to its association with drug resistance is accurate, then no association with young age and recent transmission would be expected in situations where the Beijing genotype has not (yet) acquired these high levels of drug resistance. Moreover, if a strong program is in place to deal with drug-resistant tuberculosis, this selective advantage may disappear (4).

On the basis of the observation of Prodinger et al., we see no reason to dilute our previous message regarding the emergence of Beijing genotype strains. Ongoing research suggests that the Beijing genotype strains elicit a different immune response than other *M. tuberculosis* genotypes in particular human populations. For instance, in Jakarta, Indonesia, tuberculosis patients infected with Beijing genotype strains were significantly more likely to have febrile responses during the first 2 weeks of treatment (5). In this region we again also found a significant association with INH and streptomycin resistance.

Within the framework of a Concerted Action Project of the European Union, involving 32 institutes within and outside Europe, the worldwide spread of Beijing genotype strains will be examined. We strongly favor study of the genetic makeup of the Beijing genotype to gain insight into the success of this highly conserved family of strains, which appears to be responsible for a substantial part of the worldwide recurrence of tuberculosis, and in particular, of multidrug-resistant tuberculosis.

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